

Clustal W(1.4) multiple sequence alignment

4 Sequences Aligned. Alignment Score = 12736
Gaps Inserted = 4 Conserved Identities = 308

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:

Open Gap Penalty = 10.0 Extend Gap Penalty = 0.1 ..
Similarity Matrix: blosum ..

Multiple Alignment Parameters:

Open Gap Penalty = 10.0 Extend Gap Penalty = 0.1
Delay Divergent = 40% Gap Distance = 8
Similarity Matrix: blosum

Processing time: 14.5 seconds

con3707.pep	1	MDQYCILGRIGEAGHIVFKAKHVEPRVGWQCLPSILQTGEIVALKKVAL	50
con3705.pep	1	MDQYCILGRIGEAGHIVFKAKHVEPRVGWQCLPSILQTGEIVALKKVAL	50
con3703.pep	1	MDQYCILGRIGEAGHIVFKAKHVET-----GEIVALKKVAL	37
con3702.pep	1	MDQYCILGRIGEAGHIVFKAKHVET-----GEIVALKKVAL	37
		*****	*****
con3707.pep	51	RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLSD	100
con3705.pep	51	RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLSD	100
con3703.pep	38	RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLSD	87
con3702.pep	38	RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLSD	87
		*****	*****
con3707.pep	101	LAEVVRHAQRPLAQAVKSYLQMLLKGVAFCANNIVHRDLKPANLLISA	150
con3705.pep	101	LAEVVRHAQRPLAQAVKSYLQMLLKGVAFCANNIVHRDLKPANLLISA	150
con3703.pep	88	LAEVVRHAQRPLAQAVKSYLQMLLKGVAFCANNIVHRDLKPANLLISA	137
con3702.pep	88	LAEVVRHAQRPLAQAVKSYLQMLLKGVAFCANNIVHRDLKPANLLISA	137
		*****	*****
con3707.pep	151	SGQLKIADFGGLARVFSPDGSRLLYTHQVATRWYRAPELLYGARQYDQGVDL	200
con3705.pep	151	SGQLKIADFGGLARVFSPDGSRLLYTHQVATRWYRAPELLYGARQYDQGVDL	200
con3703.pep	138	SGQLKIADFGGLARVFSPDGSRLLYTHQVATR-----	167
con3702.pep	138	SGQLKIADFGGLARVFSPDGSRLLYTHQVATRWYRAPELLYGARQYDQGVDL	187
		*****	*****
con3707.pep	201	WSVGCIMGELLNGSPLFPKGNDIEQLCYVRLILGTPNPQVWPELTELPDY	250
con3705.pep	201	WSVGCIMGELLNGSPLFPKGNDIEQLCYVRLILGTPNPQVW-----	242
con3703.pep	168	-SVGCIMGELLNGSPLFPKGNDIEQLCYVRLILGTPNPQVWPELTELPDY	216
con3702.pep	188	WSVGCIMGELLNGSPLFPKGNDIEQLCYVRLILGTPNPQVWPELTELPDY	237
		*****	*****
con3707.pep	251	NKISFKEQVPMPLLEEVLPDVSPQALDLLGQFLYYPPHQRIAASKALLHQY	300
con3705.pep	243	-----EQVPMPLLEEVLPDVSPQALDLLGQFLYYPPHQRIAASKALLHQY	286
con3703.pep	217	NKISLKEQVPMPLLEEVLPDVSPQALDLLGQFLYYPPHQRIAASKALLHQY	266
con3702.pep	238	NKISFKEQVPMPLLEEVLPDVSPQALDLLGQFLYYPPHQRIAASKALLHQY	287
		*****	*****
con3707.pep	301	FFTAPLPAHPSELPVPQRLLGGPAPKAHPGPPHIHDFHVDRPLEESLNPE	350
con3705.pep	287	FFTAPLPAHPSELPIPQRLLGGPAPKAHPGPPHIHDFHVDRPLEESLNPE	336
con3703.pep	267	FFTAPLPAHPSELPIPQRLLGGPAPKAHPGPPHIHDFHVDRPLEESLNPE	316
con3702.pep	288	FFTAPLPAHPSELPIPQRLLGGPAPKAHPGPPHIHDFHVDRPLEESLNPE	337
		*****	*****
con3707.pep	351	LIRPFILEG 359	
con3705.pep	337	LIRPFILEG 345	
con3703.pep	317	LIRPFILER 325	
con3702.pep	338	LIRPFILER 346	

FIGURE 1

Clustal W(1.4) multiple sequence alignment

4 Sequences Aligned.
Gaps Inserted = 4

Alignment Score = 42511
Conserved Identities = 932

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:

Open Gap Penalty = 10.0 Extend Gap Penalty = 5.0 ..

Multiple Alignment Parameters:

Open Gap Penalty = 10.0 Extend Gap Penalty = 5.0
Delay Divergent = 40% Transitions: Weighted

Processing time: 107.3 seconds

con3702.seq	1	ATGGACCAGTACTGCATCCTGGGCCGATCGGGGAGGG	38
con3703.seq	1	GGACCTTCTAGAATGGACCAGTACTGCATCCTGGGCCGATCGGGGAGGG	50
con3707.seq	1	ATGGACCAGTACTGCATCCTGGGCCGATCGGGGAGGG	38
con3705.seq	1	ATGGACCAGTACTGCATCCTGGGCCGATCGGGGAGGG	38

con3702.seq	39	CGCCCACGGCATCGTCTTCAGGCCAACGACGTGGAG-----	75
con3703.seq	51	CGCCCACGGCATCGTCTTCAGGCCAACGACGTGGAG-----	87
con3707.seq	39	CGCCCACGGCATCGTCTTCAGGCCAACGACGTGGAGCCGAGGGTGGCCT	88
con3705.seq	39	CGCCCACGGCATCGTCTTCAGGCCAACGACGTGGAGCCGAGGGTGGCCT	88

con3702.seq	76	-----ACTGGCGAGATAAGTTGCCCTCAAG	99
con3703.seq	88	-----ACTGGCGAGATAAGTTGCCCTCAAG	111
con3707.seq	89	GGCAGTGTCTGCCCTCTATCCTGCAGACTGGCGAGATAAGTTGCCCTCAAG	138
con3705.seq	89	GGCAGTGTCTGCCCTCTATCCTGCAGACTGGCGAGATAAGTTGCCCTCAAG	138

con3702.seq	100	AAGGTGGCCCTAACCGGGTTGGAAGACGGCTTCCCTAACCAACCAGGCCCTGCG	149
con3703.seq	112	AAGGTGGCCCTAACCGGGTTGGAAGACGGCTTCCCTAACCAACCAGGCCCTGCG	161
con3707.seq	139	AAGGTGGCCCTAACCGGGTTGGAAGACGGCTTCCCTAACCAACCAGGCCCTGCG	188
con3705.seq	139	AAGGTGGCCCTAACCGGGTTGAGGACGGCTTCCCTAACCAACCAGGCCCTGCG	188

con3702.seq	150	GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC	199
con3703.seq	162	GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC	211
con3707.seq	189	GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC	238
con3705.seq	189	GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC	238

con3702.seq	200	TGAAGGCTGTCTCCCACACGGTGGAGGCTTGTGCTGGCTTTGAGTTC	249
con3703.seq	212	TGAAGGCTGTCTCCCACACGGTGGAGGCTTGTGCTGGCTTTGAGTTC	261
con3707.seq	239	TGAAGGCTGTCTCCCACACGGTGGAGGCTTGTGCTGGCTTTGAGTTC	288
con3705.seq	239	TGAAGGCTGTCTCCCACACGGTGGAGGCTTGTGCTGGCTTTGAGTTC	288

con3702.seq	250	ATGCTCGGATCTGGCCGAGGTGGTGCGCATGCCAGAGGCCGCTAGC	299
con3703.seq	262	ATGCTCGGATCTGGCCGAGGTGGTGCGCATGCCAGAGGCCACTAGC	311
con3707.seq	289	ATGCTCGGATCTGGCCGAGGTGGTGCGCATGCCAGAGGCCACTAGC	338
con3705.seq	289	ATGCTCGGATCTGGCCGAGGTGGTGCGCATGCCAGAGGCCACTAGC	338

con3702.seq	300	CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTAACGGGTGTCGCCT	349
con3703.seq	312	CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTAACGGGTGTCGCCT	361
con3707.seq	339	CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTAACGGGTGTCGCCT	388
con3705.seq	339	CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTAACGGGTGTCGCCT	388

FIGURE 2

(FIGURE 2, cont)

con3702.seq	350	TCTGCCATGCCAACAAACATTGTACATCGGGACCTGAAACCTGCCAACCTG	399
con3703.seq	362	TCTGCCATGCCAACAAACATTGTACATCGGGACCTGAAACCTGCCAACCTG	411
con3707.seq	389	TCTGCCATGCCAACAAACATTGTACATCGGGACCTGAAACCTGCCAACCTG	438
con3705.seq	389	TCTGCCATGCCAACAAACATTGTACATCGGGACCTGAAACCTGCCAACCTG	438

con3702.seq	400	CTCATCAGCGCTCAGGCCAGCTCAAGATAAGCGGACTTTGGCCTGGCTCG	449
con3703.seq	412	CTCATCAGCGCTCAGGCCAGCTCAAGATAAGCGGACTTTGGCCTGGCTCG	461
con3707.seq	439	CTCATCAGCGCTCAGGCCAGCTCAAGATAAGCGGACTTTGGCCTGGCTCG	488
con3705.seq	439	CTCATCAGCGCTCAGGCCAGCTCAAGATAAGCGGACTTTGGCCTGGCTCG	488

con3702.seq	450	AGTCTTTCCCCAGACGGCAGCCGCCTCTACACACACCAGTGGCCACCA	499
con3703.seq	462	AGTCTTTCCCCAGACGGCAGCCGCCTCTACACACACCAGTGGCCACCA	511
con3707.seq	489	AGTCTTTCCCCAGACGGCAGCCGCCTCTACACACACCAGTGGCCACCA	538
con3705.seq	489	AGTCTTTCCCCAGACGGCAGCCGCCTCTACACACACCAGTGGCCACCA	538

con3702.seq	500	GGTGGTACCGAGCCCCCGAGCTCCTGTATGGTGCCCGCCAGTATGACCAG	549
con3703.seq	512	GGT-----	514
con3707.seq	539	GGTGGTACCGAGCCCCCGAGCTCCTGTATGGTGCCCGCCAGTATGACCAG	588
con3705.seq	539	GGTGGTACCGAGCCCCCGAGCTCCTGTATGGTGCCCGCCAGTATGACCAG	588

con3702.seq	550	GGCGTCGATCTGTGGCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGG	599
con3703.seq	515	-----CTGTGGGCTGCATCATGGGGGAGCTGTTGAATGG	548
con3707.seq	589	GGCGTCGATCTGTGGCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGG	638
con3705.seq	589	GGCGTCGATCTGTGGCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGG	638

con3702.seq	600	GTCCCCCCTTTCCCGGGCAAGAACGATATTGAACAGCAGCTTGCTATGTGC	649
con3703.seq	549	GTCCCCCCTTTCCCGGGCAAGAACGATATTGAACAGCAGCTTGCTATGTGC	598
con3707.seq	639	GTCCCCCCTTTCCCGGGCAAGAACGATATTGAACAGCAGCTTGCTATGTGC	688
con3705.seq	639	GTCCCCCCTTTCCCGGGCAAGAACGATATTGAACAGCAGCTTGCTATGTGC	688

con3702.seq	650	TTCGCATCTTGGGCACCCCCAACCTCTCAAGTCTGGCCGGAGCTCACTGAG	699
con3703.seq	599	TTCGCATCTTGGGCACCCCCAACCTCTCAAGTCTGGCCGGAGCTCACTGAG	648
con3707.seq	689	TTCGCATCTTGGGCACCCCCAACCTCTCAAGTCTGGCCGGAGCTCACTGAG	738
con3705.seq	689	TTCGCATCTTGGGCACCCCCAACCTCTCAAGTCTGGCCGGAGC-----	730

con3702.seq	700	CTGCCGGACTACAACAAGATCTCCTTAAGGAGCAGGTGCCCATGCCCT	749
con3703.seq	649	CTGCCGGACTACAACAAGATCTCCTTAAGGAGCAGGTGCCCATGCCCT	698
con3707.seq	739	CTGCCGGACTACAACAAGATCTCCTTAAGGAGCAGGTGCCCATGCCCT	788
con3705.seq	731	-----AGGTGCCCATGCCCT	746

con3702.seq	750	GGAGGAGGTGCTGCCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC	799
con3703.seq	699	GGAGGAGGTGCTGCCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC	748
con3707.seq	789	GGAGGAGGTGCTGCCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC	838
con3705.seq	747	GGAGGAGGTGCTGCCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC	796

con3702.seq	800	AATTCCCTCTCTACCCCTCCTCACCAAGCGCAGCTCCAAGGCTCTC	849
con3703.seq	749	AATTCCCTCTCTACCCCTCCTCACCAAGCGCAGCTCCAAGGCTCTC	798
con3707.seq	839	AATTCCCTCTCTACCCCTCCTCACCAAGCGCAGCTCCAAGGCTCTC	888
con3705.seq	797	AATTCCCTCTCTACCCCTCCTCACCAAGCGCAGCTCCAAGGCTCTC	846

(FIGURE 2 cont)

con3702.seq	850	CTCCATCAGTACTTCTTCACAGCTCCCCGCGCTGCCCATCCATCTGAGCT	899
con3703.seq	799	CTCCATCAGTACTTCTTCACAGCTCCCCGCGCTGCCCATCCATCTGAGCT	848
con3707.seq	889	CTCCATCAGTACTTCTTCACAGCTCCCCGCGCTGCCCATCCATCTGAGCT	938
con3705.seq	847	CTCCATCAGTACTTCTTCACAGCTCCCCGCGCTGCCCATCCATCTGAGCT	896

con3702.seq	900	GCCGATTCCCTCAGCGTCTAGGGGACCTGCCCCAAGGCCATCCAGGGC	949
con3703.seq	849	GCCGATTCCCTCAGCGTCTAGGGGACCTGCCCCAAGGCCATCCAGGGC	898
con3707.seq	939	GCCGGTTCCCTCAGCGTCTAGGGGACCTGCCCCAAGGCCATCCAGGGC	988
con3705.seq	897	GCCGATTCCCTCAGCGTCTAGGGGACCTGCCCCAAGGCCATCCAGGGC	946

con3702.seq	950	CCCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG	999
con3703.seq	899	CCCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG	948
con3707.seq	989	CCCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG	1038
con3705.seq	947	CCCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG	996

con3702.seq	1000	TTGAACCCAGAGCTGATTGGCCCTTCATCCTGGAGGGTGAGGATCCTG	1049
con3703.seq	949	TTGAACCCAGAGCTGATTGGCCCTTCATCCTGGAGAGGTGAGGATCCTG	998
con3707.seq	1039	TTGAACCCAGAGCTGATTGGCCCTTCATCCTGGAGGGTGAGGATCCTG	1088
con3705.seq	997	TTGAACCCAGAGCTGATTGGCCCTTCATCCTGGAGGGTGAGGATCCTG	1038

con3702.seq	1050	AGAA 1053	
con3703.seq	999	AGAA 1002	
con3707.seq	1089	AGAA 1092	
con3705.seq	1039	1038	